

#6

## RAW SEQUENCE LISTING

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Application Serial Number: 101522,043  
Source: PCT  
Date Processed by STIC: 1-30-05

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PATENT APPLICATION: US/10/522,043

DATE: 01/30/2005  
TIME: 10:07:01

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3 <110> APPLICANT: Lu et al.  
5 <120> TITLE OF INVENTION: Polypeptide  
7 <130> FILE REFERENCE: 69856  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/522,043  
C--> 9 <141> CURRENT FILING DATE: 2005-01-19  
9 <150> PRIOR APPLICATION NUMBER: PCT/GB03/04296  
10 <151> PRIOR FILING DATE: 2003-10-03  
12 <150> PRIOR APPLICATION NUMBER: 0306261.9  
13 <151> PRIOR FILING DATE: 2003-03-19  
15 <150> PRIOR APPLICATION NUMBER: 0223193.4  
16 <151> PRIOR FILING DATE: 2002-10-07  
18 <160> NUMBER OF SEQ ID NOS: 9  
20 <170> SOFTWARE: PatentIn version 3.1  
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28 <223> OTHER INFORMATION: p53 inhibitor peptide  
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65 <211> LENGTH: 6  
66 <212> TYPE: PRT

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 99 <213> ORGANISM: Homo sapiens  
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 106 tccagcccccc agcccccgcgg ggcccccgcgc cagcgtccca tccccctcag catatcttc 180  
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 112 caatcacaac cacagccccca gctgccccaa cagccccaga cccaaacccca aacccttacc 360  
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 116 aaccccccac cgagctggag cctgagccgg agatagaggg gctgctgaca ccagtgcgtgg 480  
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 124 ctgcccccta cccacaagaa acagtaccag cagatcatca gccgccttcc ccatcgatcat 720  
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 136 cagcccaacg aggaggcat cactgccttgc cacaacgcgc tctgcggcgc caactactt 1080  
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| 160 | gcctgggag    | gtctggaaag   | ggctggaaat             | cactggggac  | agggaaaccac | ttcctttgc   | 1800 |
| 162 | caaatcagat   | cccggtccaaa  | gtgcctccca             | tgccttaccac | catcatcaca  | tcccccagca  | 1860 |
| 164 | agccagccac   | ctgcccagcc   | gggcctggga             | tgggccacca  | caccactgga  | tattcctggg  | 1920 |
| 166 | agtcaactgt   | gacaccatct   | ctcccgagcag            | tcttgggtc   | tgggtggaa   | acattggct   | 1980 |
| 168 | ctaccaggat   | ccctgccccca  | cctctcccca             | attaagtgcc  | ttcacacacgc | actggttaa   | 2040 |
| 170 | tgtttataaa   | caaaaatagag  | aaactggtt              | aatgtttata  | aacaaaatag  | agaaactttc  | 2100 |
| 172 | gcttataaaat  | aaaagtagtt   | tgcacagaaaa            | tgaaaaaaaaa | aaaaaaaaaa  | aaaaaaaaaa  | 2156 |
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| 177 | <212>        | TYPE:        | DNA                    |             |             |             |      |
| 178 | <213>        | ORGANISM:    | Caenorhabditis elegans |             |             |             |      |
| 180 | <400>        | SEQUENCE:    | 7                      |             |             |             |      |
| 181 | atggtcacga   | ccagtagcgg   | agggggtata             | gggtacccgg  | caaacaacgg  | tgtcacacag  | 60   |
| 183 | gtgtctctga   | ttcactcgtc   | ggattctgtt             | cgaactgttt  | caactgc(cc  | aatataccgt  | 120  |
| 185 | ccgacgtcat   | caatggcatc   | tacgatggct             | cataaaatctt | cgacggctcc  | gttcatctcc  | 180  |
| 187 | gcaaataaac   | aatgtcaaa    | accggcggtt             | cgggtggtcg  | ctcaaccacc  | accaccat    | 240  |
| 189 | ccacaaggcat  | tgtcccaaca   | gtatcaccag             | cagaatccga  | tgtatgttgc  | ttccgcacca  | 300  |
| 191 | aatacacgac   | cacacgttat   | tccgacaatg             | caagtgcac   | cgacaatggc  | cgctcaaatt  | 360  |
| 193 | aaacgaaata   | atcctgttaa   | tgcacagtt              | cagaaccctt  | ctgaaaatgt  | cgccgattac  | 420  |
| 195 | gggtaaaac    | cgcagtcagt   | agaaatggtg             | caaagagttc  | gagctgttcg  | aagacaagtc  | 480  |
| 197 | gcccacgagg   | agacccaact   | gcgaagactc             | agagagtttgc | aacacgaaac  | ggcacagctt  | 540  |
| 199 | caaaaataaga  | attatggaaag  | agaaaagagag            | ttgaatgtgc  | aaggatccat  | gctaaaagaa  | 600  |
| 201 | gctcaatttag  | agttgagaaa   | tgcttcaatg             | agggcgcaat  | ctttaaacaa  | gcatttggaa  | 660  |
| 203 | gaaatgttacc  | ggagaagaca   | aactgcagca             | gcggcagcgc  | tcgtggaaaca | acgaaaaatg  | 720  |
| 205 | cagcaacatc   | agattcttct   | agcccgagct             | gcaaatcaag  | tatccacaca  | agaagttata  | 780  |
| 207 | agacctcggt   | tttctgtcga   | accattccaa             | gttaataata  | cccaacagca  | acaaccatca  | 840  |
| 209 | cctcaaatac   | tgaaatcaga   | agaattttcg             | gagaaaagag  | atttgaatgg  | acaaactggc  | 900  |
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| 213 | ttggcaccat   | gtaaaagaaaa  | ccagaaaaaa             | tactcggt    | taagtaaaat  | ggcatctacg  | 1020 |
| 215 | gatcctcatt   | caaataccatc  | ttcaccatca             | acttcttcgc  | agaaagctcc  | gacgttgc    | 1080 |
| 217 | acattttctc   | caccaagttt   | tgaacagaaaa            | atcaactcg   | ctacaatgc   | tcgggattct  | 1140 |
| 219 | ccgttcgttg   | agcgtccaaac  | atcggttgg              | gatagtctag  | acgaatcaac  | actggagaagt | 1200 |
| 221 | ggaaaagactg  | atttggtatac  | acttcgatca             | gattccctga  | aagctacgaa  | acgtcggttct | 1260 |
| 223 | tgggctgctt   | ccgaaggtac   | ttcaatgtca             | gaggcagaga  | tgattcatag  | gcttcttgat  | 1320 |
| 225 | gaacaacgtc   | gtgggagatc   | acattttatt             | ccacaattgc  | caacatcaca  | agaagaacca  | 1380 |
| 227 | tccgcaataa   | catcagaaaaac | atatgccaa              | gaagggtgtca | attcagaatc  | gaaacaagtt  | 1440 |
| 229 | gctacaagtt   | cggatccac    | taataatctt             | gaattgcca   | ccgaacaaat  | ggtatttaggt | 1500 |
| 231 | agtgataccca  | caacagaaga   | agatgcacgt             | tcgtgttca   | cacgttctga  | tgatggacag  | 1560 |
| 233 | aatcttgaaa   | tggaaagttgc  | gattgaaaga             | agaactgtt   | aaggcatttt  | gagaagacct  | 1620 |
| 235 | aatgaaaaga   | tgaacaaagg   | tgcgttgc               | tttgcacccat | tagcactt    | gctcgatgt   | 1680 |
| 237 | gcttttagaaag | gagaactcga   | ttttagtggaa            | agcagtgcct  | caaagctaac  | agatgtctca  | 1740 |
| 239 | caggccaatg   | atgaagggat   | tacggcggt              | cacaatgcga  | tttgcgttgc  | acactatgag  | 1800 |
| 241 | attgttaagat  | ttttgtatcga  | gaacgacgt              | gatgtgaatg  | ctcaagattc  | cgatgggtgg  | 1860 |
| 243 | actccacttc   | attgtcgac    | ttcctgtat              | aaccttccaa  | tggtagaca   | acttgtggaa  | 1920 |
| 245 | ggaggaggat   | gcgttctcg    | tgcacacta              | tctgatatgg  | aaacacctgt  | ggagaagtg   | 1980 |
| 247 | gaagaagatg   | aagatggta    | tgtggatgt              | ttgaagttac  | tttccgcagc  | ccataactca  | 2040 |
| 249 | acgggatcaa   | ttaataactgg  | aaaagttac              | gctgttatg   | gatatgaggg  | ggcatttgaa  | 2100 |
| 251 | gatgagctca   | gttttgcgt    | aggagatgaa             | ttgacggta   | taaagtcgt   |             | 2160 |

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 275 Val Ala Arg Val Leu Ala Glu Ile Pro Arg Pro Leu Lys Arg Arg Gly  
 276 35 40 45  
 279 Ser Met Glu Gln Ala Pro Ala Val Ala Leu Pro Pro Thr His Lys Lys  
 280 50 55 60  
 283 Gln Tyr Gln Gln Ile Ile Ser Arg Leu Phe His Arg His Gly Gly Pro  
 284 65 70 75 80  
 287 Gly Pro Gly Gly Arg Ser Gln Ser Cys Pro Pro Ser Leu Arg Asp Leu  
 288 85 90 95  
 291 Arg Pro Gly Gln Gly Pro Leu Leu Leu Pro His Gln Leu Pro Phe His  
 292 100 105 110  
 295 Arg Pro Ala Pro Ser Gln Ser Ser Pro Pro Glu Gln Pro Gln Ser Met  
 296 115 120 125  
 299 Glu Met Arg Ser Val Leu Arg Lys Ala Gly Ser Pro Arg Lys Ala Arg  
 300 130 135 140  
 303 Arg Ala Arg Leu Asn Pro Leu Val Leu Leu Asp Ala Ala Leu Thr  
 304 145 150 155 160  
 307 Gly Glu Leu Glu Val Val Gln Gln Ala Val Lys Glu Met Asn Asp Pro  
 308 165 170 175  
 311 Ser Gln Pro Asn Glu Glu Gly Ile Thr Ala Leu His Asn Ala Ile Cys  
 312 180 185 190  
 315 Gly Ala Asn Tyr Ser Ile Val Asp Phe Leu Ile Thr Ala Gly Ala Asn  
 316 195 200 205  
 319 Val Asn Ser Pro Asp Ser His Gly Trp Thr Pro Leu His Cys Ala Ala  
 320 210 215 220  
 323 Ser Cys Asn Asp Thr Val Ile Cys Met Ala Leu Val Gln His Gly Ala  
 324 225 230 235 240  
 327 Ala Ile Phe Ala Thr Thr Leu Ser Asp Gly Ala Thr Ala Phe Glu Lys  
 328 245 250 255  
 331 Cys Asp Pro Tyr Arg Glu Gly Tyr Ala Asp Cys Ala Thr Tyr Leu Ala  
 332 260 265 270  
 335 Asp Val Glu Gln Ser Met Gly Leu Met Asn Ser Gly Ala Val Tyr Ala  
 336 275 280 285  
 339 Leu Trp Asp Tyr Ser Ala Glu Phe Gly Asp Glu Leu Ser Phe Arg Glu  
 340 290 295 300  
 343 Gly Glu Ser Val Thr Val Leu Arg Arg Asp Gly Pro Glu Glu Thr Asp  
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| 370 | Val Ser Thr Ala Pro Ile Tyr Arg Pro Thr Ser Ser Met Ala Ser Thr |     |     |
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| 374 | Met Ala His Lys Ser Ser Thr Ala Pro Phe Ile Ser Ala Asn Gln Arg |     |     |
| 375 | 50 55 60  |     |     |
| 378 | Met Ser Lys Pro Pro Val Arg Val Val Ala Gln Pro Pro Pro Pro His |     |     |
| 379 | 65 70 75 80   |     |     |
| 382 | Pro Gln Ala Leu Ser Gln Gln Tyr His Gln Gln Asn Pro Met Met Met |     |     |
| 383 | 85 90 95  |     |     |
| 386 | Tyr Ser Ala Pro Asn Thr Arg Pro His Val Ile Pro Thr Met Gln Val |     |     |
| 387 | 100 105 110   |     |     |
| 390 | Gln Pro Thr Met Ala Ala Gln Ile Lys Arg Asn Asn Pro Val Asn Ala |     |     |
| 391 | 115 120 125   |     |     |
| 394 | Gln Phe Gln Asn Pro Ser Glu Met Ile Ala Asp Tyr Gly Val Lys Pro |     |     |
| 395 | 130 135 140   |     |     |
| 398 | Gln Ser Val Glu Met Val Gln Arg Val Arg Ala Val Arg Arg Gln Val |     |     |
| 399 | 145 150 155 160   |     |     |
| 402 | Ala Asp Glu Glu Thr Glu Leu Arg Arg Leu Arg Glu Leu Glu His Glu |     |     |
| 403 | 165 170 175   |     |     |
| 406 | Thr Ala Gln Leu Gln Asn Lys Asn Tyr Gly Arg Glu Arg Glu Leu Asn |     |     |
| 407 | 180 185 190   |     |     |
| 410 | Val Gln Gly Ser Met Leu Lys Glu Ala Gln Leu Glu Leu Arg Asn Ala |     |     |
| 411 | 195 200 205   |     |     |
| 414 | Ser Met Arg Ala Gln Ser Leu Asn Lys His Leu Glu Glu Met Tyr Arg |     |     |
| 415 | 210 215 220   |     |     |
| 418 | Arg Arg Gln Thr Ala Ala Ala Ala Leu Val Glu Gln Arg Lys Met     |     |     |
| 419 | 225 230 235 240   |     |     |
| 422 | Gln Gln His Gln Ile Leu Leu Ala Arg Ala Ala Asn Gln Val Ser Thr |     |     |
| 423 | 245 250 255   |     |     |
| 426 | Gln Glu Val Ile Arg Pro Arg Ala Ser Val Glu Pro Phe Gln Val Asn |     |     |
| 427 | 260 265 270   |     |     |
| 430 | Asn Thr Gln Gln Gln Pro Ser Pro Gln Met Met Lys Ser Glu Glu     |     |     |
| 431 | 275 280 285   |     |     |
| 434 | Phe Ser Glu Lys Arg Asp Leu Asn Gly Gln Thr Gly Ser Tyr Asp Ala |     |     |
| 435 | 290 295 300   |     |     |
| 438 | Ile Asp Gly Ser Gly Asp His Gln Lys Ile Pro Thr Glu Pro Ser Tyr |     |     |
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L:53 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
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